

08963656 Results

Antibody
SEQ ID NO: 2

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	355	100.0	355	19	AAW51744	Human C-C chemokin
2	308	86.8	355	17	AAW03376	CC-chemokine recep
3	308	86.8	355	18	AAW10100	Human C-C chemokin
4	228	64.2	355	17	AAW03377	CC-chemokine recep
5	228	64.2	355	18	AAW31850	Human eosinophil e
6	228	64.2	355	18	AAW27124	Human chemokine re
7	228	64.2	355	19	AAW51745	Human C-C chemokin
8	228	64.2	355	22	AAG80109	Human CCR3 protein
9	228	64.2	356	18	AAW25943	Human CCKR3 chemok
10	190	53.5	355	22	ABB56341	Non-endogenous hum
11	134	37.7	355	17	AAW03378	CC-chemokine recep
12	134	37.7	355	19	AAW51746	Human C-C chemokin
13	41	11.5	295	22	AAG80106	Human CCR1 protein
14	41	11.5	355	15	AAR52749	C-C chemokine rece
15	41	11.5	355	18	AAW26588	Human MIP-1 alpha/
16	41	11.5	355	18	AAW25751	Human MIP-1alpha/R
17	41	11.5	355	21	AAB20571	Human CC-chemokine

RESULT 15

AAW26588

ID AAW26588 standard; Protein; 355 AA.

XX

AC AAW26588;

XX

DT 21-JAN-1998 (first entry)

XX

DE Human MIP-1 alpha/RANTES receptor.

XX

KW Macrophage inflammatory protein-1 alpha; MIP-1 alpha;
 KW reduced upon activation normal T expressed and secreted; RANTES;
 KW receptor; cytokine; antiinflammatory; inflammation; human.

XX

OS Homo sapiens.

XX

PN US5652133-A.

XX

PD 29-JUL-1997.

XX

PF 28-JAN-1993; 93US-0012988.

XX

PR 28-JAN-1993; 93US-0012988.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Murphy PM;

XX

DR WPI; 1997-392945/36.

DR

N-PSDB; AAT90384.

XX

PT MIP-1-alpha and RANTES receptor nucleic acid - used to develop
 PT products for the detection of these cytokine(s) and their receptors,
 PT particularly in inflammatory processes

XX

PS Claim 2; Column 15-18; 12pp; English.

XX

CC This polypeptide comprises a claimed receptor for human macrophage
 CC inflammatory protein-1 alpha (MIP-1 alpha) and regulated upon
 CC activation normal T expressed and secreted (RANTES) protein. Also
 CC claimed are: a nucleic acid (see AAT90384) that encodes the receptor;
 CC a subsequence of the nucleic acid, having at least 12 contiguous

CC nucleotides; a cell transformed or transfected with the nucleic
 CC acid; and purified MIP-1 alpha/RANTES receptor polypeptide. The
 CC products can be used for detecting the MIP-1 alpha/RANTES receptor
 CC and polymorphisms in physiological samples. In addition, the
 CC receptor can be expressed and used to assay for MIP-1a/RANTES in
 CC biological samples. The quantitation of MIP-1 alpha/RANTES is
 CC useful for monitoring the levels of these cytokines in a patient.
 CC Such measurements are useful in following the antiinflammatory
 CC effects of drugs and prospective usefulness of new antiinflammatory
 CC agents.
 XX
 SQ Sequence 355 AA;

Query Match 11.5%; Score 41; DB 18; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.4e-31;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
 |||||
 Db 115 tglyseiffiillltidrylaivhavfalrartvtfgvitsi 155

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	228	64.2	355	4	US-08-575-967A-4	Sequence 4, Appli
2	228	64.2	355	4	US-08-847-296B-1	Sequence 1, Appli
3	228	64.2	355	4	US-09-045-583-54	Sequence 54, Appl
4	41	11.5	355	1	US-08-012-988A-2	Sequence 2, Appli
5	41	11.5	355	1	US-08-450-393A-5	Sequence 5, Appli
6	41	11.5	355	4	US-08-446-669-5	Sequence 5, Appli
7	41	11.5	355	4	US-09-045-583-53	Sequence 53, Appl
8	41	11.5	355	4	US-09-239-938-1	Sequence 1, Appli
9	41	11.5	355	5	PCT-US95-00476-5	Sequence 5, Appli
10	31	8.7	31	1	US-08-450-393A-14	Sequence 14, Appl
11	31	8.7	31	4	US-08-446-669-14	Sequence 14, Appl
12	31	8.7	31	5	PCT-US95-00476-14	Sequence 14, Appl
13	22	6.2	31	1	US-08-450-393A-13	Sequence 13, Appl

RESULT 15
 PCT-US95-00476-13
 ; Sequence 13, Application PC/TUS9500476
 ; GENERAL INFORMATION:
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
 ; TITLE OF INVENTION: PROTEIN RECEPTORS
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Robbins, Berliner & Carson
 ; STREET: 201 N. Figueroa Street, 5th Floor
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90012-2628
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/00476
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Berliner, Robert

; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-00476-13

Query Match 6.2%; Score 22; DB 5; Length 31;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 IFFIILLTIDRYLAIVHAVFAL 142
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 IFFIILLTIDRYLAIVHAVFAL 22

RESULT 13
US-08-450-393A-13
; Sequence 13, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-450-393A-13

Query Match 6.2%; Score 22; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 IFFIILLTIDRYLAIVHAVFAL 142
 |||||
 Db 1 IFFIILLTIDRYLAIVHAVFAL 22

RESULT 8
 US-09-239-938-1
 ; Sequence 1, Application US/09239938
 ; Patent No. 6329510
 ; GENERAL INFORMATION:
 ; APPLICANT: Qin, Shixin
 ; APPLICANT: Newman, Walter
 ; APPLICANT: Kassam, Nasim
 ; APPLICANT: LeukoSite, Inc.
 ; TITLE OF INVENTION: ANTI-CCR1 ANTIBODIES AND METHODS OF USE
 ; TITLE OF INVENTION: THEREFOR
 ; FILE REFERENCE: LKS97-13
 ; CURRENT APPLICATION NUMBER: US/09/239,938
 ; CURRENT FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 355
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-239-938-1

Query Match 11.5%; Score 41; DB 4; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.4e-30;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
 |||||
 Db 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	308	86.8	355	2	G02436	chemokine (C-C) re
2	41	11.5	355	2	A45177	chemokine (C-C) re
3	33	9.3	355	2	I49339	macrophage inflamm
4	33	9.3	359	2	I49341	MIP-1 alpha recept
5	22	6.2	360	2	JC2443	chemokine (C-C) re
6	22	6.2	374	2	I38450	chemokine (C-C) re
7	16	4.5	383	2	S55594	G protein-coupled
8	14	3.9	352	2	A43113	chemokine (C-C) re
9	12	3.4	356	2	I49340	MIP-1 alpha recept
10	12	3.4	360	2	A57160	chemokine (C-C) re
11	12	3.4	360	2	JC4587	chemokine (C-C) re
12	10	2.8	308	2	I50241	G protein-coupled

RESULT 9
 I49340
 MIP-1 alpha receptor like-1 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
 C;Accession: I49340
 R;Gao, J.L.; Murphy, P.M.
 J. Biol. Chem. 270, 17494-17501, 1995
 A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.

A;Reference number: I49339; MUID:95340546
A;Accession: I49340
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-356 <RES>
A;Cross-references: EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550
C;Superfamily: vertebrate rhodopsin

Query Match 3.4%; Score 12; DB 2; Length 356;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 139 VFALRARTVTFG 150
|||||||
Db 140 VFALRARTVTFG 151

RESULT 10
A57160
chemokine (C-C) receptor 4 - human
N;Alternate names: C-C CKR-4
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: A57160
R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; Wells, T.N.C.
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from a human basophilic cell line.
A;Reference number: A57160; MUID:95370289
A;Accession: A57160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-360 <POW>
A;Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
A;Note: source clone K5-5
C;Genetics:
A;Gene: GDB:CMKBR4
A;Cross-references: GDB:677463
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;40-65/Domain: transmembrane #status predicted <TM1>
F;76-97/Domain: transmembrane #status predicted <TM2>
F;112-133/Domain: transmembrane #status predicted <TM3>
F;151-175/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;243-264/Domain: transmembrane #status predicted <TM6>
F;291-308/Domain: transmembrane #status predicted <TM7>
F;29-276,110-187/Disulfide bonds: #status predicted
F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 3.4%; Score 12; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 YLLNLAISDLLF 83
|||||||
Db 77 YLLNLAISDLLF 88

SEQ ID NO: 6

%						
Result	Query					
No.	Score	Match	Length	DB	ID	Description
1	343	96.6	355	17	AAW03378	CC-chemokine recep
2	343	96.6	355	19	AAW51746	Human C-C chemokin
3	181	51.0	355	17	AAW03376	CC-chemokine recep
4	181	51.0	355	17	AAW03377	CC-chemokine recep
5	181	51.0	355	18	AAW31850	Human eosinophil e
6	181	51.0	355	18	AAW27124	Human chemokine re
7	181	51.0	355	18	AAW10100	Human C-C chemokin
8	181	51.0	355	19	AAW51745	Human C-C chemokin
9	181	51.0	355	22	ABB56341	Non-endogenous hum
10	181	51.0	355	22	AAG80109	Human CCR3 protein
11	181	51.0	356	18	AAW25943	Human CCKR3 chemok
12	134	37.7	355	19	AAW51744	Human C-C chemokin
13	41	11.5	295	22	AAG80106	Human CCR1 protein
14	41	11.5	355	15	AAR52749	C-C chemokine rece
15	41	11.5	355	18	AAW26588	Human MIP-1 alpha/
16	41	11.5	355	18	AAW25751	Human MIP-1alpha/R
17	41	11.5	355	21	AAB20571	Human CC-chemokine
18	34	9.6	34	22	AAG80053	Chemokine peptide
19	31	8.7	31	16	AAR79170	End of third trans

RESULT 14

AAR52749

ID AAR52749 standard; Protein; 355 AA.

XX

AC AAR52749;

XX

DT 30-JAN-1995 (first entry)

XX

DE C-C chemokine receptor.

XX

KW C-C CKR-1; cytokine; inflammation.

XX

OS Homo sapiens.

XX

PN WO9411504-A.

XX

PD 26-MAY-1994.

XX

PF 04-NOV-1993; 93WO-US10672.

XX

PR 10-NOV-1992; 92US-0974025.

XX

PA (GETH) GENENTECH INC.

XX

PI Horuk R, Neote K, Schall T;

XX

DR WPI; 1994-183505/22.

DR

N-PSDB; AAQ62695.

XX

PT New C-C chemokine receptor and nucleic acid - are used to develop
PT prods. for use in diagnosis and therapy of inflammation and other
PT cytokine-mediated disorders

XX

PS Claim 1; Fig 9; 90pp; English.

XX

CC The sequence is that of the C-C chemokine receptor. The sequence can
CC be used in therapeutic or diagnostic compsns. for inflammation and
CC other cytokine mediated disorders.

CC

See also AAR52750-2.

XX

SQ Sequence 355 AA;

Query Match 11.5%; Score 41; DB 15; Length 355;
Best Local Similarity 100.0%; Pred. No. 2.1e-32;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
|||||
Db 115 tglyseiffiilltidrylaivhavfalrartvtfgvitsi 155

RESULT 15

AAW26588

ID AAW26588 standard; Protein; 355 AA.

XX

AC AAW26588;

XX

DT 21-JAN-1998 (first entry)

XX

DE Human MIP-1 alpha/RANTES receptor.

XX

KW Macrophage inflammatory protein-1 alpha; MIP-1 alpha;

KW reduced upon activation normal T expressed and secreted; RANTES;

KW receptor; cytokine; antiinflammatory; inflammation; human.

XX

OS Homo sapiens.

XX

PN US5652133-A.

XX

PD 29-JUL-1997.

XX

PF 28-JAN-1993; 93US-0012988.

XX

PR 28-JAN-1993; 93US-0012988.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Murphy PM;

XX

DR WPI; 1997-392945/36.

DR N-PSDB; AAT90384.

XX

PT MIP-1-alpha and RANTES receptor nucleic acid - used to develop

PT products for the detection of these cytokine(s) and their receptors,

PT particularly in inflammatory processes

XX

PS Claim 2; Column 15-18; 12pp; English.

XX

CC This polypeptide comprises a claimed receptor for human macrophage
CC inflammatory protein-1 alpha (MIP-1 alpha) and regulated upon
CC activation normal T expressed and secreted (RANTES) protein. Also
CC claimed are: a nucleic acid (see AAT90384) that encodes the receptor;
CC a subsequence of the nucleic acid, having at least 12 contiguous
CC nucleotides; a cell transformed or transfected with the nucleic
CC acid; and purified MIP-1 alpha/RANTES receptor polypeptide. The
CC products can be used for detecting the MIP-1 alpha/RANTES receptor
CC and polymorphisms in physiological samples. In addition, the
CC receptor can be expressed and used to assay for MIP-1a/RANTES in
CC biological samples. The quantitation of MIP-1 alpha/RANTES is
CC useful for monitoring the levels of these cytokines in a patient.
CC Such measurements are useful in following the antiinflammatory
CC effects of drugs and prospective usefulness of new antiinflammatory
CC agents.

XX

SQ Sequence 355 AA;

Query Match 11.5%; Score 41; DB 18; Length 355;
Best Local Similarity 100.0%; Pred. No. 2.1e-32;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
 |||||
 Db 115 tglyseiffiilltidrylaivhavfalrartvtfgvitsi 155

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	181	51.0	355	4	US-08-575-967A-4	Sequence 4, Appli
	2	181	51.0	355	4	US-08-847-296B-1	Sequence 1, Appli
	3	181	51.0	355	4	US-09-045-583-54	Sequence 54, Appl
	4	41	11.5	355	1	US-08-012-988A-2	Sequence 2, Appli
	5	41	11.5	355	1	US-08-450-393A-5	Sequence 5, Appli
	6	41	11.5	355	4	US-08-446-669-5	Sequence 5, Appli
	7	41	11.5	355	4	US-09-045-583-53	Sequence 53, Appl
	8	41	11.5	355	4	US-09-239-938-1	Sequence 1, Appli
	9	41	11.5	355	5	PCT-US95-00476-5	Sequence 5, Appli
	10	31	8.7	31	1	US-08-450-393A-14	Sequence 14, Appl
	11	31	8.7	31	4	US-08-446-669-14	Sequence 14, Appl
	12	31	8.7	31	5	PCT-US95-00476-14	Sequence 14, Appl
	13	22	6.2	31	1	US-08-450-393A-13	Sequence 13, Appl
	14	22	6.2	31	4	US-08-446-669-13	Sequence 13, Appl
	15	22	6.2	31	5	PCT-US95-00476-13	Sequence 13, Appl
	16	22	6.2	344	3	US-08-466-343D-9	Sequence 9, Appli
	17	22	6.2	347	1	US-08-461-244-3	Sequence 3, Appli
	18	22	6.2	352	3	US-08-466-343D-2	Sequence 2, Appli
	19	22	6.2	352	4	US-09-045-583-52	Sequence 52, Appl
	20	22	6.2	360	1	US-08-450-393A-4	Sequence 4, Appli

RESULT 4

US-08-012-988A-2

; Sequence 2, Application US/08012988A

; Patent No. 5652133

; GENERAL INFORMATION:

; APPLICANT: Murphy, Philip M.

; TITLE OF INVENTION: Cloning and Expression of Human

; TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1

; TITLE OF INVENTION: alpha)/RANTES Receptor

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew

; STREET: One Market Plaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94610

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/012,988A

; FILING DATE: 19930128

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber,, Kenneth A.

; REGISTRATION NUMBER: 31,677

; REFERENCE/DOCKET NUMBER: 15280-118

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-543-9600

; TELEFAX: 415-543-5043

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 355 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-012-988A-2

Query Match 11.5%; Score 41; DB 1; Length 355;
Best Local Similarity 100.0%; Pred. No. 3.7e-31;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
|||||
Db 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155

RESULT 5
US-08-450-393A-5
; Sequence 5, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-450-393A-5

Query Match 11.5%; Score 41; DB 1; Length 355;
Best Local Similarity 100.0%; Pred. No. 3.7e-31;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
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Db 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155

RESULT 12
 PCT-US95-00476-14
 ; Sequence 14, Application PC/TUS9500476
 ; GENERAL INFORMATION:
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
 ; TITLE OF INVENTION: PROTEIN RECEPTORS
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Robbins, Berliner & Carson
 ; STREET: 201 N. Figueroa Street, 5th Floor
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90012-2628
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/00476
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Berliner, Robert
 ; REGISTRATION NUMBER: 20,121
 ; REFERENCE/DOCKET NUMBER: 5555-291
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 310-977-1001
 ; TELEFAX: 310-977-1003
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 31 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 PCT-US95-00476-14

Query Match 8.7%; Score 31; DB 5; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.3e-22;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 IFFIILLTIDRYLAIVHAVFALRARTVTFGV 151
 |||||
 Db 1 IFFIILLTIDRYLAIVHAVFALRARTVTFGV 31

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	181	51.0	355	1	CKR3_HUMAN	P51677 homo sapien
2	64	18.0	355	1	CKR3_MACMU	P56483 macaca mula
3	55	15.5	355	1	CKR3_CERAE	P56492 cercopithec
4	41	11.5	355	1	CKR1_HUMAN	P32246 homo sapien
5	41	11.5	355	1	CKR1_MACMU	P56482 macaca mula
6	33	9.3	355	1	CKR1_MOUSE	P51675 mus musculu
7	33	9.3	359	1	CKR3_MOUSE	P51678 mus musculu
8	29	8.2	358	1	CKR3_CAVPO	Q922i3 cavia porce
9	23	6.5	359	1	CKR3_RAT	O54814 rattus norv
10	22	6.2	352	1	CKR5_CERAE	P56493 cercopithec
11	22	6.2	352	1	CKR5_CERTO	O62743 cercocobus
12	22	6.2	352	1	CKR5_GORGO	P56439 gorilla gor
13	22	6.2	352	1	CKR5_HYLLE	O97883 hylobates l
14	22	6.2	352	1	CKR5_MACMU	P79436 macaca mula

RESULT 4

CKR1_HUMAN

ID CKR1_HUMAN STANDARD; PRT; 355 AA.

AC P32246;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE C-C chemokine receptor type 1 (C-C CKR-1) (CC-CKR-1) (CCR-1) (CCR1)

DE (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)

DE (RANTES-R) (HM145) (LD78 receptor).

GN CCR1 OR CMKBR1 OR CMKR1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93161416; PubMed=7679328;

RA Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.;

RT "Molecular cloning, functional expression, and signaling

RT characteristics of a C-C chemokine receptor.";

RL Cell 72:415-425(1993).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=93240122; PubMed=7683036;

RA Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,

RA Murphy P.M.;

RT "Structure and functional expression of the human macrophage

RT inflammatory protein 1 alpha/RANTES receptor.";

RL J. Exp. Med. 177:1421-1427(1993).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Monocytes;

RX MEDLINE=94092629; PubMed=7505609;

RA Nomura H., Nielsen B.W., Matsushima K.;

RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative

RT leukocyte chemotactic peptide receptors.";

RL Int. Immunol. 5:1239-1249(1993).

CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,

CC MIP-1 DELTA, RANTES, AND MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-

CC BETA OR MCP-1 AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING

CC THE INTRACELLULAR CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING

CC STEM CELL PROLIFERATION.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT HEMATOPOIETIC

CC CELLS.

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC -----

DR EMBL; L09230; AAA58408.1; -.

DR EMBL; L10918; AAA36543.1; -.

DR EMBL; D10925; BAA01723.1; -.

DR PIR; A45177; A45177.

DR GCRDb; GCR_0498; -.

DR GCRDb; GCR_0557; -.

DR GCRDb; GCR_0573; -.

DR MIM; 601159; -.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRRHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein.

FT	DOMAIN	1	34	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	35	60	1 (POTENTIAL).
FT	DOMAIN	61	64	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	65	91	2 (POTENTIAL).
FT	DOMAIN	92	107	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	108	129	3 (POTENTIAL).
FT	DOMAIN	130	146	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	147	171	4 (POTENTIAL).
FT	DOMAIN	172	197	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	198	223	5 (POTENTIAL).
FT	DOMAIN	224	239	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	240	264	6 (POTENTIAL).
FT	DOMAIN	265	281	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	282	305	7 (POTENTIAL).
FT	DOMAIN	306	355	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	5	5	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	106	183	BY SIMILARITY.
FT	CONFLICT	337	337	E -> D (IN REF. 3).
SQ	SEQUENCE	355 AA;	41172 MW;	B2C100FFED275985 CRC64;

Query Match 11.5%; Score 41; DB 1; Length 355;
 Best Local Similarity 100.0%; Pred. No. 4.2e-31;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
 ||||||||||||||||||||||||||||||||||||||||
 Db 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155

RESULT 7
 CKR3_MOUSE
 ID CKR3_MOUSE STANDARD; PRT; 359 AA.
 AC P51678;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Probable C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3)
 DE (CCR3) (CKR3) (Macrophage inflammatory protein-1 alpha receptor-like
 DE 2) (MIP-1 alpha RL2).
 GN CCR3 OR CMKBR3 OR CMKBR1L2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=96072806; PubMed=7594543;
 RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
 RA Gerard C.;
 RT "Molecular characterization of two murine eosinophil beta chemokine
 RT receptors.";
 RL J. Immunol. 155:5299-5305(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=95340546; PubMed=7542241;
 RA Gao J.-L., Murphy P.M.;
 RT "Cloning and differential tissue-specific expression of three mouse
 RT beta chemokine receptor-like genes, including the gene for a
 RT functional macrophage inflammatory protein-1 alpha receptor.";
 RL J. Biol. Chem. 270:17494-17501(1995).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,
 CC MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: DETECTED IN SKELETAL MUSCLE AND IN TRACE
 CC AMOUNTS IN LEUKOCYTES.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

```

CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U29677; AAA86118.1; -.
DR EMBL; U28406; AAA89155.1; -.
DR GCRDb; GCR_1673; -.
DR GCRDb; GCR_1695; -.
DR MGD; MGI:104616; Cmkbr112.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 38 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 39 64 1 (POTENTIAL).
FT DOMAIN 65 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 95 2 (POTENTIAL).
FT DOMAIN 96 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 151 175 4 (POTENTIAL).
FT DOMAIN 176 201 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 202 227 5 (POTENTIAL).
FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 268 6 (POTENTIAL).
FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 309 7 (POTENTIAL).
FT DOMAIN 310 359 CYTOPLASMIC (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.
FT CONFLICT 270 270 R -> S (IN REF. 2).
SQ SEQUENCE 359 AA; 41825 MW; AC11ED66E283CEAF CRC64;

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Query Match          9.3%; Score 33; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 117 LYSEIFFIILLTIDRYLAIVHAVFALRARTVTF 149
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Db 121 LYSEIFFIILLTIDRYLAIVHAVFALRARTVTF 153

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SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	ID	
1	72	20.3	72	4	Q96T96	Q96t96 homo sapien
2	56	15.8	56	4	Q96T97	Q96t97 homo sapien
3	51	14.4	355	6	Q9BDS8	Q9bds8 macaca fasc
4	41	11.5	355	6	Q9MYJ8	Q9myj8 callithrix
5	35	9.9	355	11	Q91VP9	Q91vp9 mus musculu
6	35	9.9	358	6	Q9NOM0	Q9n0m0 ovis aries
7	26	7.3	351	6	Q9MYJ9	Q9myj9 oryctolagus
8	25	7.0	355	11	Q9JLY8	Q9jly8 rattus norv
9	22	6.2	316	6	Q9TUV7	Q9tuv7 saguinus sp
10	22	6.2	334	6	Q9TUQ7	Q9tuq7 erythrocebu
11	22	6.2	339	6	Q9TQX3	Q9tqx3 mandrillus
12	22	6.2	339	6	Q9TQX2	Q9tqx2 erythrocebu
13	22	6.2	339	6	Q9TQW4	Q9tqw4 pan troglod
14	22	6.2	339	6	Q9TQW2	Q9tqw2 pongo pygma
15	22	6.2	339	6	Q9TQW0	Q9tqw0 hylobates c

16	22	6.2	339	6	Q9TQV6
17	22	6.2	339	6	Q9TQV5
18	22	6.2	339	6	Q9TQV3

Q9tqv6	colobus	gue
Q9tqv5	saguinus	sp
Q9tqv3	cercopithec	

16	22	6.2	339	6	Q9TQV6	Q9tqv6 colobus gue
17	22	6.2	339	6	Q9TQV5	Q9tqv5 saguinus sp
18	22	6.2	339	6	Q9TQV3	Q9tqv3 cercopithec

SEQ ID NO: 4

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	355	100.0	355	17	AAW03377	CC-chemokine recep
2	355	100.0	355	18	AAW31850	Human eosinophil e
3	355	100.0	355	18	AAW27124	Human chemokine re
4	355	100.0	355	19	AAW51745	Human C-C chemokin
5	355	100.0	355	22	AAG80109	Human CCR3 protein
6	281	79.2	356	18	AAW25943	Human CCKR3 chemok
7	275	77.5	355	17	AAW03376	CC-chemokine recep
8	275	77.5	355	18	AAW10100	Human C-C chemokin
9	254	71.5	355	22	ABB56341	Non-endogenous hum
10	228	64.2	355	19	AAW51744	Human C-C chemokin
11	181	51.0	355	17	AAW03378	CC-chemokine recep
12	181	51.0	355	19	AAW51746	Human C-C chemokin
13	41	11.5	295	22	AAG80106	Human CCR1 protein
14	41	11.5	355	15	AAR52749	C-C chemokine rece
15	41	11.5	355	18	AAW26588	Human MIP-1 alpha/
16	41	11.5	355	18	AAW25751	Human MIP-1alpha/R
17	41	11.5	355	21	AAB20571	Human CC-chemokine
18	34	9.6	34	22	AAG80053	Chemokine peptide
19	32	9.0	32	22	AAG80082	Chemokine CCR3 ext
20	31	8.7	31	16	AAR79170	End of third trans
21	27	7.6	28	20	AAV39255	G-protein coupled
22	26	7.3	28	20	AAV39256	G-protein coupled

RESULT 14

AAR52749

ID AAR52749 standard; Protein; 355 AA.

XX

AC AAR52749;

XX

DT 30-JAN-1995 (first entry)

XX

DE C-C chemokine receptor.

XX

KW C-C CKR-1; cytokine; inflammation.

XX

OS Homo sapiens.

XX

PN WO9411504-A.

XX

PD 26-MAY-1994.

XX

PF 04-NOV-1993; 93WO-US10672.

XX

PR 10-NOV-1992; 92US-0974025.

XX

PA (GETH) GENENTECH INC.

XX

PI Horuk R, Neote K, Schall T;

XX

DR WPI; 1994-183505/22.

DR

N-PSDB; AAQ62695.

XX

PT New C-C chemokine receptor and nucleic acid - are used to develop
PT prods. for use in diagnosis and therapy of inflammation and other
PT cytokine-mediated disorders

XX

PS Claim 1; Fig 9; 90pp; English.

XX

CC The sequence is that of the C-C chemokine receptor. The sequence can
CC be used in therapeutic or diagnostic compsns. for inflammation and
CC other cytokine mediated disorders.
CC See also AAR52750-2.
XX
SO Sequence 355 AA:

Query Match 11.5%; Score 41; DB 15; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.2e-31;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TGLYSEIFFIILLTDTRYLAIVHAVFALRARTVTFGVITSI 155
 |||||
 Db 115 tglyseiffiilltdtrylaivhavfalrartvtfgvitsi 155

RESULT 15

AAW26588

ID AAW26588 standard; Protein; 355 AA.

XX

AC AAW26588:

XX

DT 21-JAN-1998 (first entry)

XX

DE Human MIP-1 alpha/RANTES receptor.

XX

KW Macrophage inflammatory protein-1 alpha; MIP-1 alpha;
KW reduced upon activation normal T expressed and secreted; RANTES;
KW receptor; cytokine; antiinflammatory; inflammation; human.

XX

OS Homo sapiens.

XX

PN US5652133-A.

XX

PD 29-JUL-1997.

XX

PF 28-JAN-1993: 93US-0012988.

XX

PR 28-JAN-1993; 93US-0012988.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Murphy PM;

XX

DR WPI; 1997-392945/36.

DR

XX

PT MIP-1-alpha and RANTES receptor nucleic acid - used to develop
PT products for the detection of these cytokine(s) and their receptors,
PT particularly in inflammatory processes

XX

PS Claim 2; Column 15-18; 12pp; English.

XX

CC This polypeptide comprises a claimed receptor for human macrophage
CC inflammatory protein-1 alpha (MIP-1 alpha) and regulated upon
CC activation normal T expressed and secreted (RANTES) protein. Also
CC claimed are: a nucleic acid (see AAT90384) that encodes the receptor;
CC a subsequence of the nucleic acid, having at least 12 contiguous
CC nucleotides; a cell transformed or transfected with the nucleic
CC acid; and purified MIP-1 alpha/RANTES receptor polypeptide. The
CC products can be used for detecting the MIP-1 alpha/RANTES receptor
CC and polymorphisms in physiological samples. In addition, the
CC receptor can be expressed and used to assay for MIP-1a/RANTES in
CC biological samples. The quantitation of MIP-1 alpha/RANTES is
CC useful for monitoring the levels of these cytokines in a patient.
CC Such measurements are useful in following the antiinflammatory
CC effects of drugs and prospective usefulness of new antiinflammatory
CC agents.

XX

SQ Sequence 355 AA;

Query Match 11.5%; Score 41; DB 18; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.2e-31;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
|||||
Db 115 tglyseiffiilltidrylaivhavfalrartvtfgvitsi 155

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	355	100.0	355	4	US-08-575-967A-4	Sequence 4, Appli
2	355	100.0	355	4	US-08-847-296B-1	Sequence 1, Appli
3	355	100.0	355	4	US-09-045-583-54	Sequence 54, Appl
4	41	11.5	355	1	US-08-012-988A-2	Sequence 2, Appli
5	41	11.5	355	1	US-08-450-393A-5	Sequence 5, Appli
6	41	11.5	355	4	US-08-446-669-5	Sequence 5, Appli
7	41	11.5	355	4	US-09-045-583-53	Sequence 53, Appl
8	41	11.5	355	4	US-09-239-938-1	Sequence 1, Appli
9	41	11.5	355	5	PCT-US95-00476-5	Sequence 5, Appli
10	31	8.7	31	1	US-08-450-393A-14	Sequence 14, Appl
11	31	8.7	31	4	US-08-446-669-14	Sequence 14, Appl
12	31	8.7	31	5	PCT-US95-00476-14	Sequence 14, Appl
13	22	6.2	31	1	US-08-450-393A-13	Sequence 13, Appl
14	22	6.2	31	4	US-08-446-669-13	Sequence 13, Appl
15	22	6.2	31	5	PCT-US95-00476-13	Sequence 13, Appl
16	22	6.2	344	3	US-08-466-343D-9	Sequence 9, Appli
17	22	6.2	347	1	US-08-461-244-3	Sequence 3, Appli
18	22	6.2	352	3	US-08-466-343D-2	Sequence 2, Appli

RESULT 4

US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1
; TITLE OF INVENTION: alpha)/RANTES Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,988A
; FILING DATE: 19930128
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber,, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-012-988A-2

Query Match 11.5%; Score 41; DB 1; Length 355;
Best Local Similarity 100.0%; Pred. No. 6.7e-31;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
|||||
Db 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155

RESULT 5
US-08-450-393A-5
; Sequence 5, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-450-393A-5

Query Match 11.5%; Score 41; DB 1; Length 355;
Best Local Similarity 100.0%; Pred. No. 6.7e-31;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
|||||
Db 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155

RESULT 9
 PCT-US95-00476-5
 ; Sequence 5, Application PC/TUS9500476
 ; GENERAL INFORMATION:
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
 ; TITLE OF INVENTION: PROTEIN RECEPTORS
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Robbins, Berliner & Carson
 ; STREET: 201 N. Figueroa Street, 5th Floor
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90012-2628
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/00476
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Berliner, Robert
 ; REGISTRATION NUMBER: 20,121
 ; REFERENCE/DOCKET NUMBER: 5555-291
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 310-977-1001
 ; TELEFAX: 310-977-1003
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 355 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 PCT-US95-00476-5

Query Match 11.5%; Score 41; DB 5; Length 355;
 Best Local Similarity 100.0%; Pred. No. 6.7e-31;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
 |||||
 Db 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	275	77.5	355	2	G02436	chemokine (C-C) re
2	41	11.5	355	2	A45177	chemokine (C-C) re
3	33	9.3	355	2	I49339	macrophage inflamm
4	33	9.3	359	2	I49341	MIP-1 alpha recept
5	22	6.2	360	2	JC2443	chemokine (C-C) re
6	22	6.2	374	2	I38450	chemokine (C-C) re
7	16	4.5	383	2	S55594	G protein-coupled
8	14	3.9	352	2	A43113	chemokine (C-C) re
9	12	3.4	356	2	I49340	MIP-1 alpha recept
10	12	3.4	360	2	A57160	chemokine (C-C) re

11	12	3.4	360	2	JC4587	chemokine (C-C) re
12	10	2.8	308	2	I50241	G protein-coupled
13	10	2.8	327	2	S56162	MDCR15 protein - h
14	10	2.8	355	2	JC5067	G protein-coupled
15	10	2.8	372	2	S26667	G protein-coupled
16	10	2.8	374	2	S42628	G protein-coupled
17	10	2.8	374	2	S32785	G protein-coupled
18	9	2.5	177	2	PH1372	angiotensin II rec
19	9	2.5	350	2	A39445	interleukin-8 rece
20	9	2.5	352	2	G00048	fusin (LESTRA) - c

RESULT 1

G02436

chemokine (C-C) receptor 3 - human

N;Alternate names: C-C CKR-3

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000

C;Accession: G02436; A57237

R;Ponath, P.D.

submitted to the EMBL Data Library, February 1996

A;Reference number: H01272

A;Accession: G02436

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-355 <PON>

A;Cross-references: EMBL:U49727; NID:g1477560; PIDN:AAB09726.1; PID:g1477561

R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.

J. Biol. Chem. 270, 16491-16494, 1995

A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.

A;Reference number: A57237; MUID:95348056

A;Accession: A57237

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>

A;Cross-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1; PID:g1199580

A;Note: the translated sequence in GenBank entry HSU28694, release 113.0,

PIDN:AAC50469.1, differs from the published sequence in having 281-Leu

C;Genetics:

A;Gene: GDB:CMKBR3

A;Cross-references: GDB:579624; OMIM:601268

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

F;36-60/Domain: transmembrane #status predicted <TM1>

F;71-91/Domain: transmembrane #status predicted <TM2>

F;108-129/Domain: transmembrane #status predicted <TM3>

F;147-171/Domain: transmembrane #status predicted <TM4>

F;205-223/Domain: transmembrane #status predicted <TM5>

F;240-261/Domain: transmembrane #status predicted <TM6>

F;288-305/Domain: transmembrane #status predicted <TM7>

F;24-273,106-183/Disulfide bonds: #status predicted

F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 77.5%; Score 275; DB 2; Length 355;

Best Local Similarity 100.0%; Pred. No. 1.7e-273;

Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTTSLDVTVEFTGTTSSYYDDVGLLCEKADTRALMAQFVPPLYSLVFTVGLLGNNVVVMILI	60
Db	1	MTTSLDVTVEFTGTTSSYYDDVGLLCEKADTRALMAQFVPPLYSLVFTVGLLGNNVVVMILI	60
Qy	61	KYRRLRIMTNIYLLNLAISDLLFLVTLPPFWIHYVRGHNNWVFGHGMCKLLSGFYHTGLYSE	120
Db	61	KYRRLRIMTNIYLLNLAISDLLFLVTLPPFWIHYVRGHNNWVFGHGMCKLLSGFYHTGLYSE	120

```

Qy 121 IFFIILLTIDRYLAIVHAVFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELFEE 180
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 IFFIILLTIDRYLAIVHAVFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELFEE 180

Qy 181 TLCSALYPEDTVYSWRHFHTLRMTIFCLVPLLVMAICYTGIKTLRLCPSKKKYKAIRL 240
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 TLCSALYPEDTVYSWRHFHTLRMTIFCLVPLLVMAICYTGIKTLRLCPSKKKYKAIRL 240

Qy 241 IFVIMAVFFIFWTPYNVAILLSSYQSILFGNDCER 275
    ||||||||||||||||||||||||||||||||||||||
Db 241 IFVIMAVFFIFWTPYNVAILLSSYQSILFGNDCER 275

```

RESULT 2

A45177
chemokine (C-C) receptor 1 - human
N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C;Accession: A45177; I55671
R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993
A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor.
A;Reference number: A45177; MUID:93161416
A;Accession: A45177
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-355 <NEO>
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
A;Experimental source: HL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
R;Gao, J.
J. Exp. Med. 177, 1421-1427, 1993
A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpha (MIP-1alpha)/RANTES receptor.
A;Reference number: I55671; MUID:93240122
A;Accession: I55671
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-355 <RES>
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
C;Genetics:
A;Gene: GDB:CMKBR1; CMKR-1
A;Cross-references: GDB:138446; OMIM:601159
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;240-264/Domain: transmembrane #status predicted <TM6>
F;288-305/Domain: transmembrane #status predicted <TM7>
F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;24-273,106-183/Disulfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 11.5%; Score 41; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.2e-33;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
    ||||||||||||||||||||||||||||||||||||||
Db 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155

```

I49339

Query Match 9.3%; Score 33; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.9e-25;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5

JC2443

chemokine (C-C) receptor 2, splice form B - human
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemotactin 1 receptor
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C;Accession: JC2443; I38463
R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor.
A;Reference number: JC2443; MUID:94324942
A;Accession: JC2443
A;Molecule type: mRNA
A;Residues: 1-360 <YAM>
A;Cross-references: DDBJ:D29984; NID:g531246; PIDN:BAA06253.1; PID:g531247
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.
A;Reference number: A53477; MUID:94195821
A;Accession: I38463
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-360 <RES>
A;Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
F;43-70/Domain: transmembrane #status predicted <TM1>
F;81-100/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>

F;207-226/Domain: transmembrane #status predicted <TM5>
 F;244-268/Domain: transmembrane #status predicted <TM6>
 F;287-309/Domain: transmembrane #status predicted <TM7>
 F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;113-190/Disulfide bonds: #status predicted

Query Match 6.2%; Score 22; DB 2; Length 360;
 Best Local Similarity 100.0%; Pred. No. 3.7e-14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 IFFIILLTIDRYLAIVHAVFAL 142
 |||||
 Db 128 IFFIILLTIDRYLAIVHAVFAL 149

RESULT 6

I38450
 chemokine (C-C) receptor 2, splice form A - human
 N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemotactin 1 receptor
 C;Species: Homo sapiens (man)
 C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
 C;Accession: I38450
 R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.
 A;Reference number: A53477; MUID:94195821
 A;Accession: I38450
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-374 <RES>
 A;Cross-references: EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556
 C;Genetics:
 A;Gene: GDB:CMKBR2
 A;Cross-references: GDB:337364; OMIM:601267
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
 F;44-68/Domain: transmembrane #status predicted <TM1>
 F;79-99/Domain: transmembrane #status predicted <TM2>
 F;115-136/Domain: transmembrane #status predicted <TM3>
 F;154-178/Domain: transmembrane #status predicted <TM4>
 F;208-226/Domain: transmembrane #status predicted <TM5>
 F;244-265/Domain: transmembrane #status predicted <TM6>
 F;292-309/Domain: transmembrane #status predicted <TM7>
 F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;32-277,113-190/Disulfide bonds: #status predicted

Query Match 6.2%; Score 22; DB 2; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3.8e-14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 IFFIILLTIDRYLAIVHAVFAL 142
 |||||
 Db 128 IFFIILLTIDRYLAIVHAVFAL 149

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	355	100.0	355	1	CKR3_HUMAN	P51677 homo sapien
2	64	18.0	355	1	CKR3_MACMU	P56483 macaca mula
3	55	15.5	355	1	CKR3_CERAE	P56492 cercopithec

4	41	11.5	355	1	CKR1_HUMAN	P32246	homo sapien
5	41	11.5	355	1	CKR1_MACMU	P56482	macaca mula
6	33	9.3	355	1	CKR1_MOUSE	P51675	mus musculus
7	33	9.3	359	1	CKR3_MOUSE	P51678	mus musculus
8	29	8.2	358	1	CKR3_CAVPO	Q9z2i3	cavia porce
9	23	6.5	359	1	CKR3_RAT	O54814	rattus norv
10	22	6.2	352	1	CKR5_CERAE	P56493	cercopithec
11	22	6.2	352	1	CKR5_CERTO	O62743	cercocobus
12	22	6.2	352	1	CKR5_GORGO	P56439	gorilla gor
13	22	6.2	352	1	CKR5_HYLLE	O97883	hylobates l
14	22	6.2	352	1	CKR5_MACMU	P79436	macaca mula
15	22	6.2	352	1	CKR5_PANTR	P56440	pan troglod
16	22	6.2	352	1	CKR5_PAPHA	P56441	papio hamad
17	22	6.2	352	1	CKR5_PONPY	O97881	pongo pygma
18	22	6.2	352	1	CKR5_PYGBI	O97880	pygathrix b

RESULT 4

CKR1_HUMAN

ID CKR1_HUMAN STANDARD; PRT; 355 AA.

AC P32246;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE C-C chemokine receptor type 1 (C-C CKR-1) (CC-CKR-1) (CCR-1) (CCR1)

DE (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)

DE (RANTES-R) (HM145) (LD78 receptor).

GN CCR1 OR CMKBR1 OR CMKR1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93161416; PubMed=7679328;

RA Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.;

RT "Molecular cloning, functional expression, and signaling

RT characteristics of a C-C chemokine receptor.";

RL Cell 72:415-425(1993).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=93240122; PubMed=7683036;

RA Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,

RA Murphy P.M.;

RT "Structure and functional expression of the human macrophage

RT inflammatory protein 1 alpha/RANTES receptor.";

RL J. Exp. Med. 177:1421-1427(1993).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Monocytes;

RX MEDLINE=94092629; PubMed=7505609;

RA Nomura H., Nielsen B.W., Matsushima K.;

RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative

RT leukocyte chemotactic peptide receptors.";

RL Int. Immunol. 5:1239-1249(1993).

CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,

CC MIP-1 DELTA, RANTES, AND MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-

CC BETA OR MCP-1 AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING

CC THE INTRACELLULAR CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING

CC STEM CELL PROLIFERATION.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT HEMATOPOIETIC

CC CELLS.

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC or send an email to license@isb-sib.ch).

DR EMBL; L09230; AAA58408.1; -.
DR EMBL; L10918; AAA36543.1; -.
DR EMBL; D10925; BAA01723.1; -.
DR PIR; A45177; A45177.
DR GCRDb; GCR_0498; -.
DR GCRDb; GCR_0557; -.
DR GCRDb; GCR_0573; -.
DR MIM; 601159; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 60 1 (POTENTIAL).
FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 91 2 (POTENTIAL).
FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
FT CONFLICT 337 337 E -> D (IN REF. 3).
SQ SEQUENCE 355 AA; 41172 MW; B2C100FFED275985 CRC64;

Query Match 11.5%; Score 41; DB 1; Length 355;
Best Local Similarity 100.0%; Pred. No. 3.2e-31;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155
|||||
Db 115 TGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSI 155

RESULT 6
CKR1_MOUSE
ID CKR1_MOUSE STANDARD; PRT; 355 AA.
AC P51675;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C chemokine receptor type 1 (C-C CKR-1) (CC-CKR-1) (CCR-1) (CCR1)
DE (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)
DE (RANTES-R).
GN CCR1 OR CMKBR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV; TISSUE=Peritoneal macrophage;
RX MEDLINE=96072806; PubMed=7594543;
RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
RA Gerard C.;
RT "Molecular characterization of two murine eosinophil beta chemokine

RT receptors.";

RL J. Immunol. 155:5299-5305(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SVJ;

RX MEDLINE=95340546; PubMed=7542241;

RA Gao J.-L., Murphy P.M.;

RT "Cloning and differential tissue-specific expression of three mouse

RT beta chemokine receptor-like genes, including the gene for a

RT functional macrophage inflammatory protein-1 alpha receptor.";

RL J. Biol. Chem. 270:17494-17501(1995).

CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,

CC RANTES, AND LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND

CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR

CC CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL

CC PROLIFERATION.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: DETECTED IN THE HEART, SPLEEN, LUNG,

CC PERITONEAL EXUDATE CELLS AND LEUKOCYTES.

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; U29678; AAA86119.1; -.

DR EMBL; U28404; AAA89153.1; -.

DR GCRDb; GCR_1672; -.

DR GCRDb; GCR_1698; -.

DR MGD; MGI:104618; Cmkbr1.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRRHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane.

FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 35 60 1 (POTENTIAL).

FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 65 91 2 (POTENTIAL).

FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 108 129 3 (POTENTIAL).

FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 147 171 4 (POTENTIAL).

FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 198 223 5 (POTENTIAL).

FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 240 264 6 (POTENTIAL).

FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 282 305 7 (POTENTIAL).

FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).

FT DISULFID 106 183 BY SIMILARITY.

FT CONFLICT 55 55 M -> V (IN REF. 2).

SQ SEQUENCE 355 AA; 40901 MW; FCE9FFF70E6F38B1 CRC64;

Query Match 9.3%; Score 33; DB 1; Length 355;

Best Local Similarity 100.0%; Pred. No. 1.3e-23;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 GLYSEIFFIILLTIDRYLAIVHAVFALRARTVT 148

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Db 116 GLYSEIFFIILLTIDRYLAIVHAVFALRARTVT 148